

L. Helms

#10

1642

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RAW SEQUENCE LISTING DATE: 07/06/2000
PATENT APPLICATION: US/09/203,768A TIME: 13:01:24

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Output Set: N:\CRF3\07062000\I203768A.raw

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3 <110> APPLICANT: Huse, William D.
4      Watkins, Jeffry D.
6 <120> TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
7      of Use
9 <130> FILE REFERENCE: P-IX 2947
11 <140> CURRENT APPLICATION NUMBER: 09/203,768A
12 <141> CURRENT FILING DATE: 1998-12-02
14 <160> NUMBER OF SEQ ID NOS: 8
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34      1           5           10          15
36 gtc ctg tcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag 96
37 Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
38      20           25           30
40 cct tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc 144
41 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
42      35           40           45
44 agt ggt tac tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg 192
45 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
46      50           55           60
48 gag tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg 240
49 Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
50      65           70           75           80
52 tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag 288
53 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
54      85           90           95
56 ttc tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat 336
57 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
58      100          105          110
60 tac tgt gcg aga gaa ata gca gct cgt cct cac cga tac ttt gac tac 384
61 Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr
62      115          120          125
64 tgg ggc cag gga acc ctg gtc acc gtc tcc tca 417
65 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
66      130          135

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79     20          25          30
81 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
82     35          40          45
84 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
85     50          55          60
87 Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
88   65           70          75          80
90 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
91     85          90          95
93 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
94     100         105         110
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119   1           5          10          15
121 gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctc tcc tgc agg 96
122 Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
123     20          25          30
125 gcc agt cag agt gtt agc agc aac tta gcc tgg tac cag cag aaa cct 144
126 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
127     35          40          45
129 ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act 192
130 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
131     50          55          60
133 ggt atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act 240
134 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
135   65           70          75          80

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137 ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtt tat tac tgt	288
138 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys	
139 85 90 95	
141 cag cag tat aat aac tgg cct ccg tac act ttt ggc cag ggg acc aag	336
142 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
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159 Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg	
160 20 25 30	
162 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro	
163 35 40 45	
165 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr	
166 50 55 60	
168 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr	
169 65 70 75 80	
171 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys	
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178 115	
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193 1 5 10 15	
195 tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc agc tat	96
196 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr	
197 20 25 30	
199 gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg	144
200 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
201 35 40 45	
203 gga ggg atc atc cct atc ttt ggt aca gca aac tac gca cag aag ttc	192
204 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe	

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205      50          55          60
207 cag ggc aga gtc acg att acc gcg gac gaa tcc acg agc aca gcc tac 240
208 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
209   65          70          75          80
211 atg gag ctg agc acg ctg aga tct gag gac acg gcc gtg tat tac tgt 288
212 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
213           85          90          95
215 gcg aga gaa gat agc agt ggc tgg tat cac tac tgg ggc cag gga acc 336
216 Ala Arg Glu Asp Ser Ser Gly Trp Tyr His Tyr Trp Gly Gln Gly Thr
217           100         105         110
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233 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
234           20          25          30
236 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
237           35          40          45
239 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
240           50          55          60
242 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
243   65          70          75          80
245 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
246           85          90          95
248 Ala Arg Glu Asp Ser Ser Gly Trp Tyr His Tyr Trp Gly Gln Gly Thr
249           100         105         110
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252           115
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258 <213> ORGANISM: Homo sapiens
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262 <222> LOCATION: (1)..(333)
264 <400> SEQUENCE: 7
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266 Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
267   1           5          10          15
269 aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca 96
270 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
271           20          25          30
273 agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat 144

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274 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
275 35 40 45
277 ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc 192
278 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
279 50 55 60
281 agc tca gga aac aca gct tcc ttg acc atc act ggg gct cag gcg gaa 240
282 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
283 65 70 75 80
285 gat gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac ccc 288
286 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
287 85 90 95
289 gtg gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc 333
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291 100 105 110
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295 <211> LENGTH: 111
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303 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
304 20 25 30
306 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
307 35 40 45
309 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
310 50 55 60
312 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
313 65 70 75 80
315 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
316 85 90 95
318 Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
319 100 105 110

VERIFICATION SUMMARY DATE: 07/06/2000
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